

SEQUENCE LISTING

<110> DEGUSSA AG
Rieping, Mechthild
Siebelt, Nicole

<120> Process for the fermentative preparation of L-amino acids using strains of the Enterobacteriaceae family

<130> 236399US-0-X

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> Primer

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<221> Primer

<222> (1)..(30)

<223> rseB1

<400> 1

gatagcggga ttctagataa ggggtattagg

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<212> DNA

<213> artificial sequence

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<223> rseB2

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gcaacaactg cagtgaatc actgg

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<210> 3

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<212> DNA

<213> Escherichia coli

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<221> CDS

<222> (1)..(957)

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1				5					10					15		

ttc	tct	gct	aac	gcc	tcg	gcc	act	ccc	gcg	tcc	ggg	gcg	tta	tta	cag	96
Phe	Ser	Ala	Asn	Ala	Ser	Ala	Thr	Pro	Ala	Ser	Gly	Ala	Leu	Leu	Gln	
			20					25					30			

cag	atg	aac	ctg	gcc	agt	cag	tca	ctg	aat	tac	gag	ctg	tca	ttc	atc	144
Gln	Met	Asn	Leu	Ala	Ser	Gln	Ser	Leu	Asn	Tyr	Glu	Leu	Ser	Phe	Ile	
		35					40					45				

agc	atc	aat	aaa	cag	ggg	gtt	gag	tct	ctg	cgt	tat	cga	cat	gca	cgc	192
Ser	Ile	Asn	Lys	Gln	Gly	Val	Glu	Ser	Leu	Arg	Tyr	Arg	His	Ala	Arg	
	50					55					60					

ctc	gat	aac	cgt	cct	ctt	gca	caa	ttg	ttg	caa	atg	gat	ggc	ccg	cgc	240
Leu	Asp	Asn	Arg	Pro	Leu	Ala	Gln	Leu	Leu	Gln	Met	Asp	Gly	Pro	Arg	
65					70					75					80	

cgg	gaa	gtg	gta	cag	cgc	ggc	aat	gaa	atc	agc	tat	ttt	gaa	ccg	gga	288
Arg	Glu	Val	Val	Gln	Arg	Gly	Asn	Glu	Ile	Ser	Tyr	Phe	Glu	Pro	Gly	
				85				90						95		

ctt	gaa	ccg	ttc	acg	ctt	aat	ggc	gat	tac	att	gtt	gat	tct	ctg	cca	336
Leu	Glu	Pro	Phe	Thr	Leu	Asn	Gly	Asp	Tyr	Ile	Val	Asp	Ser	Leu	Pro	
			100					105					110			

tcg	ctt	atc	tat	acc	gat	ttc	aaa	cgc	ctt	tct	cct	tac	tac	gac	ttt	384
Ser	Leu	Ile	Tyr	Thr	Asp	Phe	Lys	Arg	Leu	Ser	Pro	Tyr	Tyr	Asp	Phe	
		115					120					125				

atc	tcc	gtc	ggg	cgc	acg	cgt	att	gct	gat	cgt	ctt	tgc	gaa	gtc	att	432
Ile	Ser	Val	Gly	Arg	Thr	Arg	Ile	Ala	Asp	Arg	Leu	Cys	Glu	Val	Ile	
	130					135					140					

cgc	gtg	gtt	gcc	cga	gat	ggg	aca	cgc	tac	agc	tac	atc	gtg	tgg	atg	480
Arg	Val	Val	Ala	Arg	Asp	Gly	Thr	Arg	Tyr	Ser	Tyr	Ile	Val	Trp	Met	
145					150					155					160	

gac	acc	gaa	tcg	aaa	tta	ccg	atg	cgg	gtt	gat	ctc	ctt	gat	cgc	gat	528
Asp	Thr	Glu	Ser	Lys	Leu	Pro	Met	Arg	Val	Asp	Leu	Leu	Asp	Arg	Asp	
				165					170					175		

ggt gaa acg ctg gaa caa ttt cgc gtg att gct ttt aac gtc aat cag	576
Gly Glu Thr Leu Glu Gln Phe Arg Val Ile Ala Phe Asn Val Asn Gln	
180 185 190	
gat atc agc agc agt atg cag acg ctg gcg aag gca aat ttg ccg ccg	624
Asp Ile Ser Ser Ser Met Gln Thr Leu Ala Lys Ala Asn Leu Pro Pro	
195 200 205	
ttg ctt tct gtt cct gta ggt gaa aaa gct aaa ttc agc tgg acg cca	672
Leu Leu Ser Val Pro Val Gly Glu Lys Ala Lys Phe Ser Trp Thr Pro	
210 215 220	
acc tgg ttg cca cag ggt ttt agc gaa gtt tcc agt agt cga cgt ccg	720
Thr Trp Leu Pro Gln Gly Phe Ser Glu Val Ser Ser Ser Arg Arg Pro	
225 230 235 240	
cta ccg acg atg gac aac atg cct atc gaa tca cgt ctc tat tcc gac	768
Leu Pro Thr Met Asp Asn Met Pro Ile Glu Ser Arg Leu Tyr Ser Asp	
245 250 255	
gga tta ttc agc ttc tcg gta aac gtt aac cgc gct acg cca tcg agc	816
Gly Leu Phe Ser Phe Ser Val Asn Val Asn Arg Ala Thr Pro Ser Ser	
260 265 270	
acc gat cag atg ttg cgc acc gga cgc aga acc gtc agt aca agc gta	864
Thr Asp Gln Met Leu Arg Thr Gly Arg Arg Thr Val Ser Thr Ser Val	
275 280 285	
cgt gat aac gcc gaa atc acc att gtc ggt gaa ctg ccg ccg caa acg	912
Arg Asp Asn Ala Glu Ile Thr Ile Val Gly Glu Leu Pro Pro Gln Thr	
290 295 300	
gcg aaa cgc att gcc gag aat att aag ttc ggg gca gcg caa tga	957
Ala Lys Arg Ile Ala Glu Asn Ile Lys Phe Gly Ala Ala Gln	
305 310 315	

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 <212> PRT
 <213> Escherichia coli

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Met Lys Gln Leu Trp Phe Ala Met Ser Leu Val Thr Gly Ser Leu Leu
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Phe Ser Ala Asn Ala Ser Ala Thr Pro Ala Ser Gly Ala Leu Leu Gln
20 25 30

Gln Met Asn Leu Ala Ser Gln Ser Leu Asn Tyr Glu Leu Ser Phe Ile
 35 40 45

Ser Ile Asn Lys Gln Gly Val Glu Ser Leu Arg Tyr Arg His Ala Arg
 50 55 60

Leu Asp Asn Arg Pro Leu Ala Gln Leu Leu Gln Met Asp Gly Pro Arg
 65 70 75 80

Arg Glu Val Val Gln Arg Gly Asn Glu Ile Ser Tyr Phe Glu Pro Gly
 85 90 95

Leu Glu Pro Phe Thr Leu Asn Gly Asp Tyr Ile Val Asp Ser Leu Pro
 100 105 110

Ser Leu Ile Tyr Thr Asp Phe Lys Arg Leu Ser Pro Tyr Tyr Asp Phe
 115 120 125

Ile Ser Val Gly Arg Thr Arg Ile Ala Asp Arg Leu Cys Glu Val Ile
 130 135 140

Arg Val Val Ala Arg Asp Gly Thr Arg Tyr Ser Tyr Ile Val Trp Met
 145 150 155 160

Asp Thr Glu Ser Lys Leu Pro Met Arg Val Asp Leu Leu Asp Arg Asp
 165 170 175

Gly Glu Thr Leu Glu Gln Phe Arg Val Ile Ala Phe Asn Val Asn Gln
 180 185 190

Asp Ile Ser Ser Ser Met Gln Thr Leu Ala Lys Ala Asn Leu Pro Pro
 195 200 205

Leu Leu Ser Val Pro Val Gly Glu Lys Ala Lys Phe Ser Trp Thr Pro
 210 215 220

Thr Trp Leu Pro Gln Gly Phe Ser Glu Val Ser Ser Ser Arg Arg Pro
 225 230 235 240

Leu Pro Thr Met Asp Asn Met Pro Ile Glu Ser Arg Leu Tyr Ser Asp
245 250 255

Gly Leu Phe Ser Phe Ser Val Asn Val Asn Arg Ala Thr Pro Ser Ser
260 265 270

Thr Asp Gln Met Leu Arg Thr Gly Arg Arg Thr Val Ser Thr Ser Val
275 280 285

Arg Asp Asn Ala Glu Ile Thr Ile Val Gly Glu Leu Pro Pro Gln Thr
290 295 300

Ala Lys Arg Ile Ala Glu Asn Ile Lys Phe Gly Ala Ala Gln
305 310 315